

## FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTC<sup>1</sup>CCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG  
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCGCCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT  
GGTGGACAAGTTTAAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG  
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGCTGACGGCTTCGAAGAAACG  
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT  
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC  
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA  
AACAGACTTGTATATTTTGATACAGTTCCTTGTAATAAAATTGACCATTTGTAGGTAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA  
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTT

[illegible]

><MW: 38192, pI: 4.53, NX(S/T): 2

**Signal peptide:**

**N-glycosylation sites.**

**Glycosaminoglycan attachment sites.**

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

### Casein kinase II phosphorylation sites.

**Tyrosine kinase phosphorylation site.**

**N-myristoylation sites.**

**Aspartic acid and asparagine hydroxylation site.**

**EGF-like domain cysteine pattern signature.**

Leucine zipper pattern.

amino acids 94-116

### FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGCCCGGAGGAGCGCCTTC  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC  
CGGGCCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA  
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCTTTCGCGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA  
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAACAGGATGGGGTGGCAGCATTGAAAGT  
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAAATGCTATCT  
TCTTTAAAACATGTCAACAAGCTGAGTGCCAGGCCGGGTGCCGAAATGGAGGCTTTTGTAAT  
GAAAGACGCATCTGCGAGTGTCCTGATGGGTTCACGGACCTCACTGTGAGAAAGCCCTTTG  
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC  
TGTTTCTACCCTGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCCACAACCCTGTGAAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTT  
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT  
GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCCGCCAGCTCAGGCAGC  
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCA  
TGTGTTGAATGTTCAAATAATGTTTATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT  
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTAAGTTTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTTTCTTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA  
TCAGGTTAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAATTACAATGCATTTATGGT  
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTCAGATTTTATTGTGAGATATTTAGAT  
GTTTGTTACATTTTTTAAAAATTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACC  
TTACCATTATTCCAGAGATTCAGTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATT  
AAACAATATAATATATTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGTCAT  
TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT  
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

09903925 "074404

Второй этап работы по созданию и внедрению инновационных технологий в области охраны окружающей среды и рационального использования природных ресурсов осуществляется в соответствии с программой, одобренной Советом директоров ОАО «Сибирский ЦОС».

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><subunit 1 of 1, 379 aa, 0 stop
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MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESSLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC  
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST  
TCFNNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVC  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
PESNYIW

amino acids 1-28

amino acids 88-92, 245-249

## amino acids 319-323

## amino acids 370-378

amino acids 184-190, 185-191, 189-195, 315-321

## amino acids 285-293

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGACAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG  
CCCCAGCCCCACACCTTCACCAGGGCCCAGGAGCCACCATGTGGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGAGGGTCGTGGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT  
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTTCTGGGGCATGACCCTGGATGAGGGCATTTCGCTACCGCCTGGGCACCA  
TCCGCCCATCTTCCTCGGTCATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG  
GTGCTTCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGA  
CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCTGTCTGTGCGCCCCAGAACCTGCTGTCTTGTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCCTGGTGGTTCTGCGTGC  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC  
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATAACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC  
CAGCCTGGGGCGAGAGGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAG  
AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCACTGAGGCTG  
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GGGCGGTGACCCAGCCTCGCCCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT  
CCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCCTGGGAGCCGCGGGCAGGCGAGACTGGCG  
GAGCCCCCAGACCTCCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG  
TTGCCCAGGTTGGAGTGCACTGGCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA  
AGTGACCCTCCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC  
TAATTTTTGTATTTTTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTTCGAACT  
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA  
TAAACCAAAGTATTGATAAAAAAAA

## FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC  
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR  
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

**N-glycosylation site.**

amino acids 78-82, 161-165

**Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

**N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

**Amidation site.**

amino acids 26-30, 318-322

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

00003325 "07103"

## FIGURE 7

AGGCTCCTTGGCCCTTTTTCCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCTGGGGCAAGCGCCAGGCCACTGCCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTTCCTATAACAAGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

05903925 071101

[illegible]

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGTCAGCCAGGCACTGCCCTGCTGTGCTACT  
 CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
 GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
 CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT  
 GTGACACCGACTTGTGCAACGCCAGCGGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
 GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
 CCCCCTGTCAGCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
 GCCAGTGGGAGCCTGTCCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
 CTGCACCCCTGTCCCCACCCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
 TCAGTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCTCTCTGCTGCTGTTTC  
 CATGGCCCAGCATTCTCCACCCTTAACCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT  
 CCCTGCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
 GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
 GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA  
 GGGGCCAGGCCTCACATTCTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
 AATAAACACCTGTTGGATAAGCCAAAAAAA



## FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPSSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPMPMALSRTPTRQISSDT  
DPPADGPSNPLCCCFHGPFAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

### **Signal peptide:**

amino acids 1-47

### **N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

### **N-myristoylation site.**

amino acids 56-60

### **Amidation site.**

amino acids 70-74

000039251 071101  
TTTT20 5260660

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CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAAGTCAACGGGCGTTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC  
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG  
CGTGTTACCGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCGGCACGAGG  
GCTGGTTTCATGGCCTTTCACGCGGCAGGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCACGC  
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GGCGGCCCCAGCCCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCGCCTCCC  
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC  
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CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT  
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TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTTGTGTTTGTGTTTGTGTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCACGACCCAGGCCTGCACCCCAACCCCAACTCCCAGCCC  
CGGAATAAAACCATTTTTCTGTC

# 1. Introduction

**Signal peptide:**

N-glycosylation site.

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

**Casein kinase II phosphorylation site.**

**Tyrosine kinase phosphorylation site.**

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTTTGATTTTGCTGTTTATTTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTAT  
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCT  
GAAGTCTTGGCTTATCATTTCCTTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC  
TGGATTTCTGCGAAGTGCACAATGTACAGTGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTGTCAGGAAAAC  
AATATTCAGACCATTTACGGGCTGCTCTTGGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
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AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCCTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAAATGGCTCAA  
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CCTCTCTTCACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT  
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TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
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CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT  
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATATGCACAAAAGGGGCGCTACACCTC  
CCAGAAGTGGAATAACAACCGGGGCGGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT  
CAACTCCTTAAAGGAGATTTGAGACTGCAGCCATTTACACCCCAAATGGGGGCATTAATTA  
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CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT  
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG  
CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTTGCTTTTTAAATCTT

1994, 1997, 1998, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 2159, 2160, 2161, 2162, 2163, 2164, 2165, 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175, 2176, 2177, 2178, 2179, 2180, 2181, 2182, 2183, 2184, 2185, 2186, 2187, 2188, 2189, 2190, 2191, 2192, 2193, 2194, 2195, 2196, 2197, 2198, 2199, 2200, 2201, 2202, 2203, 2204, 2205, 2206, 2207, 2208, 2209, 2210, 2211, 2212, 2213, 2214, 2215, 2216, 2217, 2218, 2219, 2220, 2221, 2222, 2223, 2224, 2225, 2226, 2227, 2228, 2229, 2230, 2231, 2232, 2233, 2234, 2235, 2236, 2237, 2238, 2239, 2240, 2241, 2242, 2243, 2244, 2245, 2246, 2247, 2248, 2249, 2250, 2251, 2252, 2253, 2254, 2255, 2256, 2257, 2258, 2259, 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269, 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279, 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289, 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298, 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308, 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318, 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328, 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337, 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347, 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357, 2358, 2359, 2360, 2361, 2362, 2363, 2364, 2365, 2366, 2367, 2368, 2369, 2370, 2371, 2372, 2373, 2374, 2375, 2376, 2377, 2378, 2379, 2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388, 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398, 2399, 2400, 2401, 2402, 2403, 2404, 2405, 2406, 2407, 2408, 2409, 2410, 2411, 2412, 2413, 2414, 2415, 2416, 2417, 2418, 2419, 2420, 2421, 2422, 2423, 2424, 2425, 2426, 2427, 2428, 2429, 2430, 2431, 2432, 2433, 2434, 2435, 2436, 2437, 2438, 2439, 2440, 2441, 2442, 2443, 2444, 2445, 2446, 2447, 2448, 2449, 2450, 2451, 2452, 2453, 2454, 2455, 2456, 2457, 2458, 2459, 2460, 2461, 2462, 2463, 2464, 2465, 2466, 2467, 2468, 2469, 2470, 2471, 2472, 2473, 2474, 2475, 2476, 2477, 2478, 2479, 2480, 2481, 2482, 2483, 2484, 2485, 2486, 2487, 2488, 2489, 2490, 2491, 2492, 2493, 2494, 2495, 2496, 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565, 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640, 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655, 2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670, 2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 26

**Signal peptide:**

**Transmembrane domain:**

N-glycosylation site.

**Casein kinase II phosphorylation site.**

**Tyrosine kinase phosphorylation site.**

N-myristoylation site.

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

### Phospholipase A2 aspartic acid active site.

amino acids 39-50

# FIGURE 14

ACTTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCGCCTCCCACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCTGCC  
TCGCTTCCAGGCGCGGCGGCTGCAGCCTTGCCCTTCTTGCTCGCCTTGAAAATGGAAAAGATGCTCGCAGGCT  
GCTTTCTGCTGATCCTCGGACAGATCGTCTCTCCCTGCCGAGGCCAGGGAGCGGTACGTGGGAGGTCCATCT  
CTAGGGGCGAGACAGCTCGGACCCACCCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAAAGCGGGCAGACC  
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA  
TCTTGCAATTCTTGGACATTGGTCTGATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGAATG  
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA  
GGGAGAATGTGCCACGGGTCAATATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA  
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAATTTAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGCAAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
GTGCCATTGAGGACCAACTGTGAGCAGCTCTGTGTGAATGTGCCGGCTCCTTCTGTCTGCCAGTGTACAGT  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAACACGGATGTGAAC  
ATGAGTGTGTAAATGCTGATGGCTCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAAA  
CGTGCAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTCTGTCTGCCAGTGTCTCAGAAGGCTTCC  
GATCAACAGGAGACCTCAAGACCTGCTCCCGGTGGATTACTGCTGAGTGACCATGTTGTGAATACTCCT  
GTGTCAACATGGACAGATCCTTTGCTGTCACTGTCTGAGGGACACGTGCTCCGACGCGATGGGAAGACGTGTG  
CAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAACATTCTGTGTGAAGCAGTGAAGATTCTGTTGTGT  
GCCAGTGTCTTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATAACGTGCGAGTGTCTGGAGGGATTCCGGCTCG  
CTGAGGATGGGAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCCAACACATTTGTGTGA  
ATAATGGGAATTCCTACATCTGCAAAATGCTCAGAGGGATTGTCTTAGCTGAGGACGGAAGACGGTGCAAGAAAT  
GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGGAGTGC  
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTGAACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTTACCCAAG  
GAGAAGGGGCCAGGCCCCCTTTCCACAAGGGTGCCGAGAGCAGCATTGTGTTACCGACGGACGGGCTCAGGATG  
ACGTCTCCGAGTGGGCCAGTAAAGCCAAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAACATAAGAGATTGCCTCTGAGCCACAAACAAGCATCTCTTCTATGCCGAAGACTTCAGCACAAATGG  
ATGAGATAAGTGAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
CAGGGGAACCTGCCAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT  
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT  
TCCAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC  
TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT  
GAACGCAGTGACAGAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGA  
GAAACCTGGTTTGGCACAGAACAAAGACAAGAAGTATACACTAATTTGTATAAATTTATCTAGGAAAAAAATCCT  
TCAGAATTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC  
AATTGCTTCTGCCTCATCTGCCTTAGTGTGCAATCTCATTGACTATACGATAAAGTTTGCACAGTCTTACTT  
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG  
CATAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTTATACAATATTAAATTCACCACTTCAG

05903525 1074104

[illegible]

**Signal peptide:**

**N-glycosylation site.**

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

Casein kinase II phosphorylation site.

N-myristoylation site.

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCTGACTCCGTCCCGGCCAGGGAGGGC  
CATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCCAGCTGCAACTGCACTTGCCCGCCAACCGGTGTCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACAGGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT  
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCCACCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTTCTTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC  
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCCAGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC  
TTATTAAACTAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAA  
TGTTTGTATGAAAAA

090325 07101



## FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPVGVANVTLSQCSPRSKPAVQYQ  
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA  
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLPPWKSSDTISKNGTL  
SSVTSARALRPPHGPFRPGALTPTPSLSSQALPSRLPTTDGAHPQPIPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 245-267

### **N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

### **N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

090395.0740

[illegible]

AA

## FIGURE 19

03003925 0710  
MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIITYIEILAESSSLLGYKNNTISAKDTL  
SNSTLTEFVKTVNNFVQRDTFVVDKLSVNHRRTHTKLMHTVEQATLRISQSFQKTTEFDT  
NSTDIALKVFFFDSDYNMKHIHPHMNMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF  
WNYSPTMTNGSWSSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAICIFTFFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL  
LHYFFLAFAWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT  
TKVCWLSTENNFISFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

### **N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### **Glycosaminoglycan attachment site.**

amino acids 49-53

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

### **Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### **Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

### **N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTTATATTATAAGAGTAT  
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA  
GGAGTCTATGTGGCATTGTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTTACCTTC  
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

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## FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCCGGCTGGGA  
CAAGAAGCCGCGCCTGCCTGCCCGGGCCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGCCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCCGGAG  
CCGCGCGCGCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGCAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGGAAGTGCAGCGCGGGGC  
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCCCTGGAGACCGACAGCATG  
GACCCATTTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT  
GAGACCATGCCCCGGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTTGCCCAGCTGCTGCCTGGGCCCCCATTTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTTGAGAATCCCC  
CTGAGGCCAGTTCTGTCTATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC  
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCTCCCCATGGATTGGGGCCT  
CCCAGGCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC  
CCTTTCCCCAGCACTTGGTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTATGTATGTAAGTGAGGTTTG  
TTTTGTATATTAAATGGAGTTTGTGTTGT

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## FIGURE 22

MRS GCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

**Signal peptide:**

amino acids 1-22

**Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

**N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

0303025.0748  
78740" 5250550

[illegible]

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA  
AGAAGACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTCCGAGTGTCTCCTTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATAACAATGAATACAAAACCTGGAAGT  
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTC  
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG  
CCGCGGCGGGCGGATCACGAGGTGAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC  
CATCTCTACTAAAATACAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA  
AATAAATACTGGTTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

## **FIGURE 24**

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQOTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDLNI SGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETS FQKSNSSSKATTMS ENVQWLTPVIPALWKAAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230

09003925 07404  
TOT 40" 52650560



## FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCAT  
CATGCTGCTATTCTCTGCAAATACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA  
TTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTTTGGACAATG  
CAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCA  
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTG  
TGGAATCCTTAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTTAACTTTCCAGCCAGATTGCC  
AGCTAACACACAGATTCTTCTCTACAGACTAACAATATTGCAAAAATTGAATACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAAT  
ATTAATGTAAAAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAACAACTTACTGA  
ACTGCCTGAAAAATGTCTGTCCGAAGTGAAGCAACTTACAAGAACTCTATATTAATCACAACT  
TGCTTTCTACAATTTACCTGGAGCCTTTATTGGCCTACATAATCTTCTTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAGAGAT  
TCTGATGATTGGGGAAAATCCAATTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCA  
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT  
GGACTGGAAAACCTTAGAAAGCATCTCTTTTTTACGATAACAGGCTTATTAAGTACCCCATGT  
TGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTGGATCTAAATAAAAATCCTATTAATAGAA  
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAATAATATGCCT  
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC  
TACTAACACCCCTAGATTGTCTTACATTCACCCCAATGCATTTTTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG  
CCAAACCTCAAGGAAATCAGCATAACAGTAACCCCATCAGGTGTGACTGTGTGCATCCGTTG  
GATGAACATGAACAAAACCAACATTGATTCATGGAGCCAGATTCAGTGTGCGTGGACC  
CACCTGAATTCCAAGGTGAGAATGTTGCGCAAGTGCATTTTCAGGGACATGATGGAAATTTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT  
TTCCTTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAAACCTCTTGCTTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA  
GATATAAATGGCGTAACCTCCCAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG  
GCTCTTTGAATATTAAAATAAGAGATATTGAGCCAATTCAGTTTTTGGTGTCTTGGAAGCA  
AGTTCTAAAATTCTCAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATTCTCA  
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTTGTATTGATATTTCCACCATCTATCAGAAAAACAGAAAAAA  
TGTGTAAATGTCACCACCAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGAATAATAC  
CACAACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA  
GCTGCCTCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG  
AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA  
AGAAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT  
AAAAACCACCAAGGAAACCTACTCCAAAATGAAC

**Q**uestions are asked about the following:

**Signal sequence:**

**Transmembrane domain:**

N-glycosylation site.

**Casein kinase II phosphorylation site.**

**Tyrosine kinase phosphorylation site.**

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

## FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC  
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA  
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG  
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC  
AACGTGATCTGTAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCCGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA  
GTAGTTTGCGATTGCAGTAGAAATAAGTGTTTACTTCTCCCATCCATTGTAAACATTTGAA  
ACTTTGTATTTTCAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA  
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT  
AATTTAAAAGCAAATAAAAGCTTAACTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

0903925.074104

$$f_{\text{eff}} = \frac{\sum_{i=1}^n f_i}{n}$$

**Signal sequence:**

**Transmembrane domain:**

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

# FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCGAGGTGAGCAAGAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT  
GGGCTCAGTGCTGTGAGGCTCGGCCACGGGCTGCCC GCCCGCTGCGAGTGCTCCGCCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG  
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCCGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCCGGCG  
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT  
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCTCACC GCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT  
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC  
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC  
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCTCAACCTCTCCTACAACCCCATCA  
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC  
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA  
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGCGCTCCTGTGGGTGTTCCGG  
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCCACGTGCGCCACGCCCCGAGTTTGTCCA  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACTGCGCGCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGACGTTT  
GTGTGCCGGGCGATGGCGACCCGCGCCCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC  
TCCATGCCCCGCCACCTGCATGTGCGCAGCTACTCGCCCCACTGGCCCCATCAGCCCAACAA  
GACCTTCGCTTTCATCTCCAACCAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG  
TGCCTTTCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC  
CTGGGCGTCGTCCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC  
AAAGCACAAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG  
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCCGGGGCGGGGGCAGGGACCCCCG  
GGCGGCCGGGCAGGGGAAGGGGCCTGGTCCGACCTGCTCACTCTCCAGTCTTCCCACCTC  
CTCCCTACCCTTCTACACAGTTCTCTTTCTCCCTCCCGCCTCCGTCCCCTGCTGCCCCCG  
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA  
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA  
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT  
TATGAAAACCTTGAAATAATAAAAAGAGAAAAAACTAAAAA AAAAAAAAAAAAAAAAAA

09903925 "074404

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEEELELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA  
FSGLNSLEQLTLEKCNLTSLIPTEALSHLHGLIVLRRLHNLNINAIRDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMMLHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLLEESVFHSGNLETIILDSNPLA  
CDCRLLWVFRRRWRLNFNRRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPFPAILWLSPRKHLVSAKSNGRLLTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGNDSPAHHLHVRYSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKGN TKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 556-578

### **N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

### **Tyrosine kinase phosphorylation site.**

amino acids 590-598

### **N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC  
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCCGGGGATTTCAGGCTCGCCAGCGCCCAGCC  
AGGGAGCCCGGCCGGGAAGCGCGATGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC  
TGTTTCGCCTGCTGCTGGGCGCCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGCCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTG  
CTCATCATGCTCATCTTCCCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCCACTTCTGCTG  
GCCCCCAGGGGCCCCCTGTGGGGACTGCTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA  
CCGAGGGCCGCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC  
TTTGGGTGCGGTTTTGTACTCGGTTTGGAATGGGGAGGGAGGGCGGGGGAGGGGAGGG  
TTGCCCTCAGCCCTTCCGTGGCTTCTCTGCATTTGGGTTATTATTATTTTGTAAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACA  
AACAAAAACA

0990352507404

## FIGURE 32

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSISISNVALADEGEYTCSTFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRI QEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

090395 "07404  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ



[illegible]

GGGGTTAGGAGGAAGGAATCCACCCCCACCCCCCAAACCTTTTCTTCTCCTTTCCTGG  
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT  
GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA  
TCTGTTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA  
AGTCTGCAGCGTTTCACTGCCCCGACTTCCAGTTTTACCATTATTTCTGCATGGCAATTTC  
CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGACATGG  
AAAACAATGGCTTGCATGAAATCGTTCGGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGC  
CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA  
TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCCTTCCAGG  
ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTACCTGCCAAC  
GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC  
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCTT  
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCCAAGAATGCC  
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG  
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG  
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
CAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA  
GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCCAGGGTCTGGGTTTAAAGATGAAC  
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA  
GCTTTTCTTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA  
ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACTTTCAAG  
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA  
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
TCCTCCCGGGCACTTTCAATGCCATGCCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG  
CTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA  
CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA  
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA  
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT  
TAGAAAGGATTTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTGGCGGAGACCGGGACGCACTCC  
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT  
GTTTGTACCTCCGCCTTCACCGTGGTGGGCATGCTCGTGTATTATCTGAGGAACCGAAAGC  
GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCCTACAGACAGTCTGT  
GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG  
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG  
ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTAACCAAATCCCCGCG  
CCATCAGCCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTCGCACAAACCGAAAGGGCCT  
GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA  
GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCAGCACGACCCTGCTGGAAG  
AACTGACAGTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC  
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTGTGGATTAG  
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT  
TGTAATAAGTAACTTTGACTTCTGAC

## FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH  
LFLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKNIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPEYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPKLRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK  
IPGNWQIKIRPTAAIATGSSRNKPLANSRPCPGGCSCDHIPGSGLMNCNNRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY  
LDTLSREKFAGLQNLLEYLNVEYNAIQILIPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLVFVTSFTTVVGMVLFILNRNKRKRDRDANSSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

### Signal sequence:

amino acids 1-15

### Transmembrane domain:

amino acids 618-638

### N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

### Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

### N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

00903925.07404

## FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGC  
CGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTCGGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCTCAG  
AGAATGAGGCCGGCGTTTCGCCCTGTGCCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCCGGCGG  
CGGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGGCCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG  
GCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGCACTGGAGCGCAGGCGTTCCCACT  
GCACCCTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAAGTCTTGTGTCTGCGCCGCGCCCCGGG  
GCCGCCTCTAACTTGAGCTATCGCGCGCCCTTCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG  
CTTTGCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA  
GTGGGGAAGGACAGCCGACCTTTGGGGGGACCGGGGTGCCACCAGGCGCCCGCCGGCCACT  
GCAACCAGCCCCGTGCCGAGAGAACATGGCCAATCAGGGTGCAGGAGAAGCTGGGAGAGAC  
ACCACTTGTCCCTGAACAAGACAATTCAGTAACATCTATTCTGAGATTCTCGATGGGGAT  
CACAGAGCACGATGTCTACCCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCCAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT  
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT  
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCCCTCTTCCCAGCCA  
AGGAAGGAGTCTATGGGCCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCTTGCTGGCGGAGTCCCCCTCTTGGCTCTAGTGATGCATAGGGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTTTTCACTTTTGTATGAAACGGGGAACCAAGAGGAACTTAC  
TTGTGTAAC TGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCCTTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA  
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA  
TTTGGAGAAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACAATATAATTTACA  
TTAAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTTCAGGCTAGGAGTAT  
ATTGGTTCGAAATCCCAGGGAAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

## FIGURE 36

MRPAFALCLLWQALWPGPGGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCTIADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPPIRVDEKLGETPLVPEQDNSVTISIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR  
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 399-418

### **N-glycosylation site.**

amino acids 189-193, 381-385

### **Glycosaminoglycan attachment site.**

amino acids 289-293

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

### **Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

### **N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

69903925 074404  
T00T20 52620659

## FIGURE 37

CGGACGCGTGGGATTTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC  
CCCCGGCTACCTGGGCGCGCCCGCGGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA  
GGGGCGTGTGTGCCGGCGCGCGCGCCGTGGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTTTCACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTTCTGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG  
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC  
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTCAGT  
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA  
AACTGCCTACAACACAGAACAGCCTGTCACCACCACATTCCCTGTAACCACGGGTTTAA  
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTTCAGCAGGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC  
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC  
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG  
TAACAGTGAACGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT  
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT  
TGCTGCTGTGTCAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGAT  
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT  
GTTATTTGTTTACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA  
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAAAAAAAAA

09903925.074404

## FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFCTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVLNFRFIDLESNDLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKKLPPTTTEQPVTTTFPVTTGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

### **Signal sequence:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 355-359

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

### **Tyrosine kinase phosphorylation site.**

amino acids 199-208

### **N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### **Cell attachment sequence.**

amino acids 149-152

05903925-0740  
TGTZQ"525E0550

[illegible]

AAGGTCTTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

$\frac{d^2x}{dt^2} = -\frac{g}{L} x$        $x(0) = 0$        $x(\pi) = 0$

**Signal sequence:**

**Transmembrane domain:**

**N-glycosylation site.**

cAMP- and cGMP-dependent protein kinase phosphorylation site.

**Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

**EGF-like domain cysteine pattern signature.**

amino acids 181-193



## FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT  
GCCACCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTACGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG  
CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCCCGCTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTGCCTCGCAGGGGGC  
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCGGAGAACTGGGTGCTGGAGCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTAAGGAGGCTCCAGCCATTAGGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTTCGAGGGTACCAGGAGAGCTG  
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA  
GAGCCCTTGCTCAGTTTTTCTCTATTCTTATTATTACTGCACTATATTCTAAGCACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTTACTTGTCTGTGTCAC  
TGGATCTGGGCTAAAGTCCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT  
AAAA

09903925 "07.4.04

**Figure 1**

**Signal sequence:**

**N-glycosylation site.**

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

**Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

## FIGURE 43

0903925 "04404

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGGACAAA  
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT  
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT  
GAATCCCACAACAGGAGAGCTGGTCTTTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGGTATCGTGGCAGCCGTCTTGTAAACCCTGATTCTCCTGGGAAT  
CTTGTTTTTTGGCATCTGGTTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGGCCTGGTCCGCTCACCGCCTATCATCTGCATTTGCCTTACT  
CAGGTGCTACCGGACTCTGGCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC  
ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCCTGGAACCTTGTTTTAAA  
GTGTTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGCAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTTCCTTGTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG  
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGTCCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTCGGGATCAGCCTGACCA  
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRI PENNPVKLS CAYSGFSSPRVEW  
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYS RGHFDR TKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

00003925 071101

## FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGAGGCCCCAGCTCAG  
GCTCGTGCCCACCCACCAAGTTCCAGTGCCGCACCAAGTGGCTTATGCGTGCCCTCACCTGG  
CGCTGCGACAGGGACTTGGAAGTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA  
GTGACTGCTCTGGGGGAAGTGCACAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCAATCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC  
CTCCGCCCCTGGGGTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC  
CTCGCTGCCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

090395.07464

$\mathbb{R}^{n_1 \times n_2}$  and  $\mathbb{R}^{n_3 \times n_4}$  are the input and output spaces, respectively, and  $\mathbb{R}^{n_1 \times n_2 \times n_3 \times n_4}$  is the space of the 4D tensors.

**Signal sequence:**

**Transmembrane domain:**

N-glycosylation site.

**Casein kinase II phosphorylation site.**

N-myristoylation site.

**Prokaryotic membrane lipoprotein lipid attachment site.**

Leucine zipper pattern.

amino acids 17-39

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 210. *Diagrams*  
 211. *Charts*  
 212. *Graphs*  
 213. *Tables*  
 214. *Figures*  
 215. *Photographs*  
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 225. *Charts*  
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 227. *Tables*  
 228. *Figures*  
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 230. *Maps*  
 231. *Diagrams*  
 232. *Charts*  
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 234. *Tables*  
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 239. *Charts*  
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 241. *Tables*  
 242. *Figures*  
 243. *Photographs*  
 244. *Maps*  
 245. *Diagrams*  
 246. *Charts*  
 247. *Graphs*  
 248. *Tables*  
 249. *Figures*  
 250. *Photographs*  
 251. *Maps*  
 252. *Diagrams*  
 253. *Charts*  
 25

CCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGACAGCAGAGGTCGCGCACAGATGCGG  
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT  
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA  
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGCATGAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTTATTATGTCGCGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT  
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG  
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGTCT  
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAACGTGTGGTGGAGTTTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTTCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGA  
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCCTTTCCCCCAGGGGGCCTCCCCGGAG  
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA  
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA  
GTCTGTATTACCTCCAGGTGCCAAGAGAGACCCACCCTGCTTCGGACAACCCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCCCTGGGT  
GTTGTTCCCTAAGAACTGATTGATTAAAAAATTTCCCAAAGTGTCCTGAAGTGTCTCTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCTTTCTTCTTGGTTTTAGACAAATGTAAACAA  
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTTCTTCTTGACACAGACTGATTAAAAAATTTAAAGNAAAAAA

## FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDQSPPAYPGSGD TDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 325-344

### **N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

### **Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### **N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

00003325.074404



1. The first part of the paper is devoted to the study of the asymptotic behavior of the solutions of the system (1) as  $t \rightarrow \infty$ . It is shown that the solutions of the system (1) tend to zero as  $t \rightarrow \infty$  if and only if the matrix  $A$  is Hurwitz.

1. The first part of the paper is devoted to the study of the asymptotic behavior of the solutions of the system (1) as  $t \rightarrow \infty$ . It is shown that the solutions of the system (1) tend to zero as  $t \rightarrow \infty$  if and only if the matrix  $A$  is Hurwitz.

[illegible]

**Signal sequence:**

**Transmembrane domain:**

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTGCACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCAAATC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTGAGAAGTCTTGATCCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGATACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTTTGACCACAAATGGCCACCGTTTGCT  
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCTTTATACAATG

650395 " 67464

$$\begin{array}{ccccccc} \Gamma_{\text{red}}^{(0)} & \Gamma_{\text{red}}^{(1)} & \Gamma_{\text{red}}^{(2)} & \Gamma_{\text{red}}^{(3)} & \Gamma_{\text{red}}^{(4)} & \Gamma_{\text{red}}^{(5)} & \Gamma_{\text{red}}^{(6)} \\ \parallel & \parallel & \parallel & \parallel & \parallel & \parallel & \parallel \\ \Gamma_{\text{red}}^{(0)} & \Gamma_{\text{red}}^{(1)} & \Gamma_{\text{red}}^{(2)} & \Gamma_{\text{red}}^{(3)} & \Gamma_{\text{red}}^{(4)} & \Gamma_{\text{red}}^{(5)} & \Gamma_{\text{red}}^{(6)} \end{array}$$

**Signal sequence:**

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

Casein kinase II phosphorylation site.

**Tyrosine kinase phosphorylation site.**

N-myristoylation site.

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA  
GTCCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA  
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA  
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTGC  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCTGCTCAGTGAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACATACATCA  
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAGGATAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAAGATAGCAC  
TATGTGTTCAAA

090325 07101

# 2025 RELEASE UNDER E.O. 14176

**Signal sequence:**

**Casein kinase II phosphorylation site.**

N-myristoylation site.

Amidation site.

**Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTTCGGCTGCCTGGG  
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC  
GACATACTTGTCACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA  
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA  
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACACT  
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTGCAGCTTATAATGGTTAC

090325-0740

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQKMSI  
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

09903925-07404  
T0T20-5260660



**Table 1** *Summary of the data sets used in the study*

CCACGCGTCCGCTGGTGTTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAA  
 AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC  
 CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTAA  
 GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA  
 GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG  
 CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT  
 GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA  
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA  
 GGCATTTCTTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG  
 CTGGACATGTCTCGGTCCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA  
 TTTCATAAAACTTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
 TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA  
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
 ATTTTTATTCCATCTTCTATAGCTTTTTTAAACAACATTGGAAAGGATCCTTCCTGAGCGTTT  
 CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA  
 AAGCGCAATAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA  
 ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTTCTTCAATA  
 TCATTTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT  
 ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
 CCAAAATGACTTTATTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
 AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTTGATTGCACTTAAATTTTGT  
 ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA  
 TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACTCTCAATGGGTAGGTTTC  
 ATCCTACCCATTGCCACTCTGTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT  
 GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG  
 GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
 AA  
 AA

# 2025

**Signal sequence:**

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

**Casein kinase II phosphorylation site.**

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

[illegible]

AAAATATTATATATAAAAGTAAAAAAAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL  
VGPFPGGLNMKSYAGFLT VNKTYSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVT SNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F  
FQIFPEYKNND FYVTGESYAGKYVPAIAH LIHSLNPVREV KINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMN NYKVLIYNGQLDIIVAAALTE RSLMGMDWKGSQEYKKA EKKVWKIFKSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFD MINRFIYGKGWDPYVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

09503555.07101

## FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT  
TTTTCCCTTTCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCCTGCCTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCCTAATATCAAATTGACTGGCTGGG  
TGAACCTCAACAGCCTTTTAACCTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCTTGAACATTCTTAAGAGGGAGAAAGTATGTTAAAAATA  
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCTGGGTC  
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTT  
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCCAGCAGCCGGC  
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT  
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA  
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCTGTCCA  
GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT  
CTTCTACATCTACGGCTTTGCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG  
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCCTGCCCTTCGGCTGCACCCGGGC  
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC  
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG  
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTT  
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC  
ATTACCTCCTCAGCAAAGAGTCCCTCTTGGAAGGTAGCTATTGGTGGAGATTTAACTATAG  
GCAACTTTATTTTCTTGGGGAACAAAGGTGAATGGGGAGGTAAGAAGGGGTAAATTTTGTG  
ACTTAGCTTCTAGCTACTTCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTTCCCAAACCTTTAAGAAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

**Abstract**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

# FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGCAGGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAACACGCGATGACCA  
 CGTGAGACCTCCGGCGGAGGCCCGGCCCGCACGCTGGGACTCCTGCTGCTGGTTCGTTGGGCTTCTGGTGTCTCC  
 GCAGGCTGGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA  
 ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT  
 GGAGGGACCGCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCTCACCACCTATGTTCCGTGGAACCTGCATG  
 AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTTCGTCTGATGGCCGCAGAGATCG  
 GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGGCCAGCTGGCTAC  
 TCCAAGACCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACC  
 TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG  
 GTTCCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACCTGC  
 TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT  
 CAACACACGAGCTGCAGCTACTGACCACCTTTCTTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT  
 ACTGGACGGGGTGGTTGACTCGTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT  
 CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG  
 GAGCCATGCATTTCCATGACTACAAGTCAAGTGTCAAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG  
 ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
 ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC  
 TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTT  
 TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG  
 TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
 ACACCGTGTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG  
 GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA  
 GCTTCTTTTCAAGGTTTCGGCCTGGACAAATGNGTTCCCTCCAGAAACACCCACATTACCTGCTTTCTTCTTGG  
 GTAGCTTGTCCATCAGCTCCACGCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA  
 TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAAGACGCTTTACCTCCAGGTCCCTGGTTGA  
 GCAGCGGAATCAACCAGGTCATCGTTTGTGAGGAGACGATGGCGGGCCCTGCATTACAGTTACCGGAAACCCCC  
 ACCTGGGCAGGAACAGTACATTAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGGCAGTGGGAGACTGCCGCCTC  
 CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG  
 ACTGGGGGCTACAGTCTGCCCCGTGCTCAGCTCAAAACCTTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGCC  
 TGGCTTTGTTGATGATGGCTTTCTACAGCCCTGCTCTTGTGCGGAGGCTGTGCGGCTGTCTCTAGGGTGGGAGC  
 AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGCTGAAACGTGCCCTTGACCCGACGTACAGCCC  
 TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTTGCTGGTTTCTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT  
 TTTATCCCCGAAATCCTGGGTGTGTACCAAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT  
 CTTCTTCAACACCTTCTGAGCCTTCTTTGGGATTCTGGAAGAACTCGGCGTGAGAAACATGTGACTTCCCCTT  
 TCCCTTCCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCTGCGTCTTCC  
 CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA  
 CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC  
 AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA  
 GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG  
 ACAGAAGGCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGGCAGAGCAGCCCTCCTTC  
 GAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGA  
 GTTGCAGTAAAGCTATAACCTTGAATCAAA

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amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586



# FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGTCCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA  
GGCAGACACTCGGTGCTTCGTAGTGGATAGGGGTCTAGACCGGTTTCTCCTAGACGGGGCCC  
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCGGAC  
CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTTATGTGCCCTGGAACTA  
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC  
AGATCCAGACTTCCTTGCCGCAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC  
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTTCAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCCGTGCACTGCTAGG  
AGAAAAGATCTTGCTCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATAACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAATCTTTACCTTGCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGTGTAAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG  
AATGGTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCCAT  
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC  
GAACCTATATGACCCATAACATTTTTGAGCCAACACCATTCCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAG  
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG  
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTTCCCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT  
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC  
ACAACAGACCCCTCTACGTGCCAAGATTCCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA  
CATTGCTGGAAGTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCCTTTCAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAAAGGTAGGCCGGGCATGGTGGCTCATGC  
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTAAAAATACAAAATTAGCCGGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAAAA

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## FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRL LKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLA AVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFS YMRHLA GLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVD FGPADNMTKIF  
TLLRKYE PHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNM MYMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSGVGD TFLYL  
PGWTKGQVWINGFNLGRYWKQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

### **Signal sequence:**

amino acids 1-27

### **N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

### **Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

### **Tyrosine kinase phosphorylation site.**

amino acids 191-198

### **N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

00003925 07104

## FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT  
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT  
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT  
CTTGTCAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG  
AAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG  
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCCAGAAGCTAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA  
TGCTTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTACATAATGACGGCAC  
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTGCTGAGCTGGAACCTCCAGA  
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT  
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAACGACT  
GACTTGTTTTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA  
AAAACCTTGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT  
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTCGGATGCTCAAGAAAAGCGGGCTTGTTG  
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCCTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AATTCCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG  
ATACATCTTTTAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTCCAAATCATTTTTTTTTTTCTTTTGGGG  
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTTAAATTGTTTGTAACTTGGAT  
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAAAAAAAAAAAAAA

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## FIGURE 68

MAYMLKKLLISYISIIICVYGFICLYTLFWLFRIP LKEYSFEKVREESSFSDIPDVKNDF AFL  
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISRNAQDKQELHLFMLS G  
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH  
VKFTDVAEIPAWVYLLKNLRELYLIGNL NSENNKMIGLES LRELRLHLKILHVKS NLTKVPSN  
ITDVAPHLT KLVIHNDG TKLLVLNSLKKMMNVAE LELQNC ELERIPHAIFSLSNLQELDLKS  
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLQ  
KLRCLDVSNNISMIP IEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP  
EKVGQLSQLTQLELKGNC LDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP  
FANGI

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

### **Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

### **Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

### **N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

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# FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTTGCATTTCCATTCCCTTTTCATTGACAAACTGACTTTTTTTTATTTCT  
TTTTTTCCATCTCTGGGCCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT  
CTGTGTTTTGGGGTTTCTTCTTCCCTCCCTGACATTGGCATTGCTTAGTGTTGTGTGGGGAGGGAGACCAGTGG  
GCTCAGTGCTTGCTTGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCCTGTC  
ATCGCTGGTGGTATCCTGGCGGCCTTGCTCCTGCTGATAGTTGTCGTGCTCTGTCTTTACTTCAAATAACACAAC  
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAACCCAGACAAGGTGTGGTGGGCCAAG  
AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTGTCTGCTGCGCTGCAAGTGTGTGAAGGATATAGAATGTGTGCC  
AGTTTTGATTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCACAGAAGAAAGGCACAG  
CTCCCATCAGTTTTCATGGAAAATAACTCAGTGCCTGCTGGGAACCCAGCTGCTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCCTCACTGTGGGGAATGCTGATAAACAGTCA  
CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAAGTACGTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCTATAAAAGCTGTGCGTCCCTTAAGGCTGCCAGCGCCTTGCCAAAATGGAGCTTGTA  
AGAAGGCTCATGCCATTGACCTCTTAATTCTCTCCTGTTTGGCGGAGCTGACAATGGCGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAAGACCAGAAAACAAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCCTCTGCTAGGG  
CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT  
GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCTAACATCTCTATTCCAAACTGT  
GGCGGTTACCTGGATACCTTGAAGGATCCTTCACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT  
TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAACTTCAAAGAGATTTTCTTAGAAATAGAC  
AAACAGTGCAAATTTGATTTTCTTGCCATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT  
GGCCGTGTGACTCCACCTTCGAATCGTCATCAAACCTCTCTGACTGTGCTGTTGTCTACAGATTATGCCAATTCT  
TACCGGGGATTTTCTGCTTCTTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGCTCTTCT  
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCAACTAAAA  
GACCCAACTTGACAGACCAAATTTATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA  
AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCCTCAACTTCTGAAGTGATCACC  
CGTCAGAAACAACCTCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA  
GAAGATGATGTAATACAAAGTCAAATGCACTGGGCAATATAACACCAGCATGGCTCTTTTGAATCCAATTCA  
TTTGAAGAGACTATACTTGAATCACCATATTATGTGGATTTGAACCAAACCTCTTTTGTTCAGTTAGTCTGCAC  
ACCTCAGATCCAAATTTGGTGGTGTCTTGTATACCTGTAGAGCCTCTCCACCTCTGACTTTGCATCTCCAACC  
TACGACCTAATCAAGAGTGGATGTAGTGCAGATGAACTTGTAAAGGTGTATCCCTTATTTGGACACTATGGGAGA  
TTCCAGTTTAATGCCTTTAAATTTCTGAGAAGTATGAGCTCTGTGTATCTGCAGTGTAAGTTTGTATGTGAT  
AGCAGTGACCACCAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAAACGAGACATTTCTTCATATAAATGG  
AAAACAGATTCATCATAGGACCCATTCTGCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAGGATTTTCAGCAT  
GAAACACATGCGGAAGAACTCCAAACCAGCCTTTCACAGTGTGCATCTGTTTTCTTCATGGTTCTAGCTCTG  
AATGTGGTGACTGTAGCGACAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACTACAAATACCAGAAGCTG  
CAGAACTATTAACTAACAGGTCCAACCCTAAGTGAGACATGTTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTATGAATAAATGAGGAAGGGCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

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## FIGURE 70

MELVRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLGOVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKSYLEAFNSNGNNLQLKDPTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLI CDSSDHQSRCNQGCVSRSKRDISSYKWKTDIIIGPIRLKRDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 571-586

### **N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

### **Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

### **N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

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TCTZQ"525E0560

## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGCTGC  
TGCTGCCGCCGCCGCGTGCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC  
CTGGACGCCCCGAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG  
GGGAGTGTTCCTGCGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA  
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT  
TTTGGAACCACTATTTACAGCAAAATTTTTTAATGCCAACCAAGTGGGCAGATATTTTTCAGGC  
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT  
CAGAATATTCGTGGAAGTGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAAGTACCTGCGTTTGGACTGTACTATTCCCTTTTGA  
ATGGTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT  
ATATAATGAAAGCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
TCTGTAAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA  
CATAAATGGGAAAACATGCATGACAATAGACAAAACGTCTCTGGGGCTATAGGAGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG  
GAGGAAATCTTTTGATGAATATTGGGGCCACACTAGATGGCACCATTCTGTAGTTTTTGGAG  
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA  
TACCTGGCGATCCAGAATGACACTGTCACCCACAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT  
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG  
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTATCAGATGC  
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTCCCACTA  
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACTTTGCCATTAAAGTC  
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT  
TTTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAA  
GTTTTTCTTTCTTCAATTATAAATTAACATAAGTGTACTGTAACCTTACAAACGTTTTAATT  
TTTAAACCTTTTTGGCTCTTTTGTAAATAACACTTAGCTTAAACATAAACTCATTGTGCAA  
ATGTAA

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## FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEFWFWYQKEKI PKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRDRLRFGLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSKPKEKLVYAI FLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295

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# FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGC  
AGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGGAGA  
TGGATTTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT  
ACTTGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT  
ACTCTACAATACCTGCCCTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAATTGATTTGTGTACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC  
TGAACCATTTGTTGAAAATAAAGCAGCATTTCAAGAATGAAGCTGCTGGGTGGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGAATTTGC  
TATGTCAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA  
AACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA  
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTTCTTTTCATGCTCC  
TTACCCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT  
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC  
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC  
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTGCAAAGTGCAA  
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGAC  
CCTTCTTTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGTCCTTCTGAGCCCGGTA  
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA  
ATCACTGTTTGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT  
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA  
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTCA  
GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTTATTTTTGCTGAGACTAATCTT  
ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG  
TACATTGTTACCTCTATATACCAAAGCACATTTTAAAAGTGCCATTAACAAATGTATCACTA  
GCCCTCCTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA  
AGCATTTAGAAAACCTT

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[illegible]

**Signal sequence:**

**Transmembrane domain:**

N-glycosylation site.

Casein kinase II phosphorylation site.

**Tyrosine kinase phosphorylation site.**

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGCGGGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAA  
ACTGCCGCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT  
TCTTTTCTTCCGCTTGGATATTTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA  
TTGGTCTAATGACTGCCAATCATTGCCCCCTATCTATGCTGACCTCTCCCTTAAATACAAC  
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC  
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG  
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTCAGA  
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATT  
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG  
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG  
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAACCTGTTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAAATGGTTTTCCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATC  
AGCTATTACAGACATCTCCATGGTTTTCTCCATGAAACTCTGTGGTTTTCATCATTCCTTCTTAG  
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA  
CGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC  
TTCATTAAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG  
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCAC  
TAACCCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATT  
TCCTTTTG

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# 2025年12月10日

**Signal sequence:**

**Transmembrane domain:**

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

**Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## FIGURE 77

GGACAGCTCGCGGCCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG  
GGGCCCCAGCCTGGCCCCGGGTACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA  
TTGCTCCTGCTGCCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGAGACCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAGCT  
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT  
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCA  
ACGGGCGCTACCAGTTCAACTTCCACGAGGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG  
GTGGCCTCCTTTGAGCAGCTCTTCCGGGCCCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCGGTGGCC  
CAGGCCTGGCACCTGGCGTGCGAAGCTACGGCCCCCGCCACCGCCGCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC  
AGCTCTTTGCCGCTGGAAGTTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGGGT  
CCGAAGCTTTGGCTTCCCCGACCCGCAGAGCCGCTTGACGGTGTTTACTGCTACCGCCAGC  
ACTAGGACCTGGGGCCCTCCCCTGCCGCATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT  
CGTTTTCCCTTGTGGGTGGAGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT  
TTAAACATTTTTTTTACTATTTTTTTGTAAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG  
GATGCCCCACTCCAGGAATCATGCTTGCTCCCCCTGGGCCATTTGCGGTTTTGTGGGCTTCTG  
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCAGAGTGGGC  
GGTGGCCTGTCTAGAATGCCGCCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCT  
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCCTCCGGAGCTGGGCTTTGGGCCTCTCCTGCC  
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAACTCCCCTCCCCGTTCCCCT  
TCCCCTCTCGGTTCCAAAGAATCTGTTTTGTTGTCAATTGTTTCTCCTGTTTCCCTGTGTGG  
GGAGGGGGCCCTCAGGTGTGTGTACTTTGGACAATAAATGGTGCTATGACTGCCTTCCGCCAA  
AA  
AA

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## FIGURE 78

MGLLLLVLPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRR LHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

### Signal sequence:

amino acids 1-17

### Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

### Tyrosine kinase phosphorylation site.

amino acids 137-145

### N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

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## FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA  
CTTCCAGTACGACCATGAGGCTTTCCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGACCGCATGGACCGCGCGGGGGAC  
GGCGACGGCTGGGTGTCGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA  
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG  
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCCGGTGAAGAATTTTCATGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC  
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG  
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCCTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA  
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG  
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCCAGGACCAGCCC  
CTGGTGGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA  
AGCGGAAATCCTGGGTAAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG  
CACAATGACCGGAGGAGGGGCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCGCAGGAG  
GCAGATGCAGTCCCAGGCATCCTCCTGCCCCTGGGCTCTCAGGGACCCCCTGGGTGCGCTTC  
TGTCCTGTGACACCCCCAACCCAGGGAGGGGCTGTCATAGTCCCAGAGGATAAGCAATAC  
CTATTTCTGACTGAGTCTCCCAGCCCAGACCCAGGGACCCTTGGCCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCT  
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA  
AAGCCAGCGCCGGGACCTTGAAA  
AAAAAAAAAAAAAAAAA

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amino acids 325-330



# FIGURE 81

GGGGCCTTGCCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
 GCGGCGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCAG  
 CCTGTCTGTCGTCGTTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTGACACCGATCCTG  
 GGCTTCGCTCGATTTGCCGCCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
 CGGGTCGTCTGTGTCCTCTCTCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCT  
 GAGGAGGTGACGCGCGGGGCTCCCGCACCCCTGGCCTTGCCCGCATTCTCCCTCTCTCCAG  
 GTGTGAGCAGCCTATCAGTCACCATGTCCGAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG  
 TGTCTGCTGCTGCTGCCGGGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTTGCTATCACATG  
 TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGGCTGCC  
 CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
 GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC  
 TGGTCGAGAAAATATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT  
 GGTCTGCTTCTTTACAGTAATAAAGGCCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
 GTGTCCACAGCACATCCACCAACAGGTAACGACTAAAGAAAACACCCGAGAAGAAAATGG  
 CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC  
 GCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA  
 GAAGGACCACATGTGGGCCTTGTTCAAGCCAGTGAACATCCCAAATAGAATTTTACTTGAA  
 AAATTTACATCAGCCAAAGATGTTTTGTTTGGCATAAAGGAAGTAGGTTTCAGAGGGGGTA  
 ATTTCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTTCTTACGGTAGATGCTGGA  
 GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT  
 CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA  
 AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGT  
 CGGAATAATGGCTTCTTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA  
 GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
 CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC  
 ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT  
 AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTTCACTGACTATAGCACCA  
 AAGAGAATGTCCTAGCTGTCATCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT  
 GATGCCATTTCCCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAA  
 CTTCTAGTAATTGTACAGATGGGCAGTCCATGATGATGTCCAAGGCCCTGCAGCTGCTG  
 CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG  
 AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCAAGAGAGTTTACAGGATT  
 AGAACCAATTGTTTCTGATGTCATCAGAGGCATTGTAGAGATTTCTTAGAATCCAGCAAT  
AATGGTAACATTTTGACAACCTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT  
 CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAATATTAAGTATGTCAAC  
 AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT  
 ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAACTCAGGAAAGAGGA  
 GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
 TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

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 253. **Abstract</**

**Signal sequence:**

N-glycosylation site.

**Casein kinase II phosphorylation site.**

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

# FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCGAGCCC  
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG  
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCCACCCTGCTGTGCCTGC  
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCGGCCCCGGCTCTCAGCTACCCGAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA  
GGTTGAGGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTAT  
CACAATGAGACCAACACAGACACGAAGGTTGGAATAATACCATCCATGTGCACCCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCAGC  
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA  
TGGCCACCAGGGGCGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG  
TGCTGTGCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA  
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG  
GAGCCTTGAGCCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT  
GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA  
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTACA  
TCTTCTTCCCAGTAAGTTTCCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTACG  
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC  
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG  
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTTTTGGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAA  
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCGAGTTCTTTCCATGGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCATCC  
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC  
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCAATTGTTCTCCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT  
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA  
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG  
GTCAAACATAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC  
AGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT  
TGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCATAACAGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA  
TAAGCATGCTTTCTTTGAGTTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC  
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

03903925 071101

[illegible]

**Signal sequence:**

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Amidation site.

amino acids 140-144

## FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGGCTCAGAAGGACTCTG  
AAGATAACAATAATTTTCAGCCCATCCACTCTCTTCCCTCCCAACACACATGTGCATGTACACACACATACA  
CACACATACACCTTCTCTCTTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTATAGAAAAGGACAC  
TAAAGCCTTAAGGACAGGCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTGAGTCAAAAAACATGGGAGGGG  
CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTCTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTGAGGAG  
TTCGAGACCAGCCTGGCCAACATGGAGAAACCCCATCTCTACTAAAAATACAAAAATTAGCCAGGAGTGGTGGC  
AGGTGCCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGT  
CAGCTGAGTGCACCGCTGCATCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACAAACACGGGAGGA  
GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACCTCTGCATCCTCTTCTTCCAGGGCTGCCCCTGATGGGGCCTG  
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGACCCCCG  
GTGTAGAATGACTGCCCTGGGAGGGTGGTTTCTTGGGCCCTGGCAGGGTTGCTGACCCTTACCCTGCAAAACACA  
AAGAGCAGGACTCCAGACTCTCTCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC  
ACTCTTGCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCCGTGGTACCCTGGCATGTTCCCTGCCCCCTCA  
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCCGCTCGTCTTACCAGGAGGTACCCTGTGGACTGCAATGA  
CCTATTCTGACGGCAGTCCCCCGGCCTCCCCGAGGCACACAGACCTGCTCCTGCAGAGCAACAGCATTGT  
CCGTGTGGACCAGAGTGAAGTGGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTTCGGA  
TGCCCGAGACTGTGATTTCATGCCCTGCCCGAGCTGCTGAGCCTGCACCTAGAGGAGAACCAGCTGACCCGGCT  
GGAGGACCACAGCTTTGACGGGCTGGCCAGCCTACAGGAACCTATCTCAACCACAACCAGCTCTACCGCATCGC  
CCCCAGGGCCTTTTCTGGCCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCCTGAGGGCCATTGACAG  
CCGCTGGTTTGAATGCTGCCCAACTTGAGATACTCATGATTGGCGGCAACAAGGTAGATGCCATCTGGACAT  
GAACCTTCCGGCCCCCTGGCCAACCTGGCTAGCCTGGTGCTAGCAGGCATGAACCTGCGGGAGATCTCCGACTATGC  
CCTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTCCTTCTATGACAACCAGCTGGCCCCGGGTGCCAGGCGGGCACT  
GGAACAGGTGCCCCGGGCTCAAGTTCCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGC  
CAACATGCTGCACCTTAAGGAGCTGGGACTGAACAACATGGAGGAGCTGGTCTCCATCGACAAGTTTGCCCTGGT  
GAACCTCCCCGAGCTGACCAAGCTGGACATACCAATAACCCACGGCTGTCTTCATCCACCCCCGCGCCTTCCA  
CCACCTGCCCCAGATGGAGACCTCATGCTCAACAACAACGCTCTCAGTGCTTGACACAGCAGCGGTGGAGTC  
CCTGCCCAACCTGCAGGAGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGTATCCGCTGGGCAATGC  
CACGGGCACCCGTGTCCGCTTCATCGAGCCGCAATCCACCCTGTGTGCGGAGCCTCCGGACCTCCAGCGCCTCCC  
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTTGCCCCCTCATCTCCCCACGAAGCTTCCCCCAAG  
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCTGATTGCCGGGCACTGGCCGAACCCGAACCCGAGATCTACTG  
GGTCACTCCAGCTGGGCTTCGACTGACACCTGCCCATGCAGGCAGGAGGTACCGGGTGTACCCCGAGGGGACCTT  
GGAGCTGCGGAGGGTGACAGCAGAAGAGGCAGGGCTATACACCTGTGTGGGCCAGAACCTGGTGGGGGCTGACAC  
TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCTCCAGCCAGGCAGGACGGAAGGACAGGGGCTGGAGCTCCG  
GGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTTGGGTACCCCAACCAACACAGTGTCCACCAACCTCAC  
CTGGTCCAGTGCCTCCTCCCTCCGGGGCCAGGGGGCCACAGCTCTGGCCCGCTGCCTCGGGGAACCCACAGCTA  
CAACATTACCCGCTCCTTCAGGCCACGGAGTACTGGGCCTGCCTGCAAGTGGCCTTTGCTGATGCCACACCCA  
GTTGGCTTGTGTATGGGCCAGGACCAAGAGGGCACTTCTTGCCACAGAGCCTTAGGGGATCGTCTGGGCTCAT  
TGCCATCCTGGCTCTCGTGTCTTCTCCTGGCAGCTGGGCTAGCGGCCACCTTGCCACAGGCCAACCCAGGAA  
GGGTGTGGGTGGGAGGCGGCTCTCCCTCCAGCCTGGGCTTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTTGT  
GTCTGCTCCCCTCGTCTGCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGGAGACACTGTTGCC  
ACCATTGTCTCAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTTTACCAA  
AGAGAAGCAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGGCTGGCAGCTGGGC  
CAAGACAGATGGGGCTTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGCCCTTACCTCCTAGGGTCA  
CCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCCTGCCCTCCCCTCTT  
CTCTCTGCCAGAGGCTCCTGGGCCTGGCTTGGCTGTCCCTACCTGTGTCCCCGGGCTGCACCCCTTCTCTT  
TCTTTCTCTGTACAGTCTCAGTTGCTTGTCTTGTGCTCCTGGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC  
CTCGGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAA  
CGCCTCATCTCAGCAGCCTGGGCTCGGCATTCCGAAGCTGACTTTCTATAGGCAATTTTGTACCTTTGTGGAGAA  
ATGTGTACCTCCCCAACCCGATTCACTCTTTTCTCCTGTTTTGTAAAAAATAAAAAATAATAACAATAAA  
AAAA

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## FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLTLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ  
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKDFALVNLP  
ELTKLDITNNPRLSFIHPRAFHHLPMETLMLNNNALSALHQQTVESLPNLQEVGLHGPNIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAEAGLYT  
CVAQNLVGADTKTVSVVVGRALLQGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRV  
SAPLVLPWNPGRKLPSSSEGETLLPPLSQNS

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 629-648

### **N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

### **Tyrosine kinase phosphorylation site.**

amino acids 532-540

### **N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

### **Amidation site.**

amino acids 470-474, 660-664, 692-696

0950355.0740  
TCTZQ 5350550

[illegible]

ATCTATAACAGAAAAAAAAAAAAAA

[illegible]

**Transmembrane domain:**

**N-glycosylation site.**

cAMP- and cGMP-dependent protein kinase phosphorylation site.

**Casein kinase II phosphorylation site.**

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447



## FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT  
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG  
AATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT  
TGCCTTGGGTGATTCTCCTGGATCTCCCCTGTTGATTTCGGTGTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGGTGAAGTTCTATAACATCTTAACTAAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGTCAGCGC  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAAATTATTCCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTG  
GGTGCGGAAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGGAAAGGCCCTGT  
ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGAAGTCAAGAAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT  
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

090325 0740Z

## FIGURE 90

MELALRRSPVPRWLLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAV NKGLYRE  
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQORDALS  
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDPKSLETS AFVKSYKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

03903955 071104

[illegible]

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACCTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG  
TTA<sup>1</sup>CTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTCACCTAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCCATCATAAACA  
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG  
GTTTGTGCTGGCAACGCCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG  
GTCGGCCCAATCGGCCCCGGTGTCTACACCAATATCAGCCACCACCTTTGAGTGGATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT  
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGGCCTACCTGAGCCCATGCAGCCTGGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGT<sup>2</sup>TTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1. *Staphylococcus aureus* (Staph aureus) is a common cause of skin infections, such as abscesses and impetigo. It is also responsible for more serious infections like pneumonia and sepsis.

**Signal sequence:**

amino acids 78-84

$\frac{d}{dt} \left( \frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}$

TGTAAGAAA

## FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAOKCHSVITQDFLTCWL  
SIRQAELLPLGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMASAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGLFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

### **Signal sequence:**

amino acids 1-16

### **N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

### **Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

### **Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

### **N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

[illegible][illegible]

**Q3636** **IN** **2011**

**Signal sequence:**

N-glycosylation site.

**Glycosaminoglycan attachment site.**

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177



## FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGCTGCCCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCCTGTGTATTCTTGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA  
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCCTTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCCGAC  
GGCCTCAGGCCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCAC  
GACTTCCGGCCCCGCCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTAT  
AGGTATTTGTAACCCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATT  
CTCCAAAAAAAAA

$$\frac{d}{dt} \left( \frac{1}{2} m \dot{x}^2 \right) = \frac{d}{dt} \left( \frac{1}{2} m \dot{y}^2 \right) = \frac{d}{dt} \left( \frac{1}{2} m \dot{z}^2 \right) = \frac{d}{dt} \left( \frac{1}{2} m \dot{\theta}^2 \right) = \frac{d}{dt} \left( \frac{1}{2} m \dot{\phi}^2 \right) = \frac{d}{dt} \left( \frac{1}{2} m \dot{\psi}^2 \right)$$

MVVSGAPPALGGGCLGTF~~T~~SLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQ~~K~~NGTHHCAGSLLTSRWVITA~~A~~HCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGV~~A~~  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC  
QVDGAWLLAGIISWGE~~G~~CAERNRPGVYISLSA~~H~~RSWVEKIVQGVQLRGRAQGGGALRAPSQ~~G~~  
SGAAARS.

amino acids 1-32

amino acids 62-66, 96-100, 214-218, 382-386; 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

amino acids 826-830

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

amino acids 607-615

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCTTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC  
AACAAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC  
CCAACCTTCCCTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC  
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCCCAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCCAAGATGTCCCTGACAGGGGCAAG  
GGAACCTCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG  
AGGTCTTGCCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACTCTGCCACCGCTAA  
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTTGAATGGGATACCACTCAAAGGG  
TGAAGAGGTCAGCTGTCCTCCTGTCATCTTCCCCACCCTGTCCCCAGCCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGGCTGTCTGCCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG  
TGTAAGTGGGGATGGGGATTCTTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC  
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT  
GTCCAACCTGTGAAA

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## FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERGRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVVWAKTERIGCGSHFCEKLGVEETNIELLCVNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRATEASDSRKMGTTPSSLATGIPAFLVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLLPLVLGIF

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

### **Glycosaminoglycan attachment site.**

amino acids 439-443

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

### **N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

### **Amidation site.**

amino acids 82-86, 172-176

### **Peroxidases proximal heme-ligand signature.**

amino acids 287-298

### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

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# FIGURE 101

GTAAGTGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAAATTCGGTCATTCTCCAAGTTATGGTGGACGT  
 ACTTCTGTTGTTCTCCCTCTGCTTGTCTTTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTTCAT  
 CAAGGCAAGTTCATGAGCCACCTTCAAAGCCTTCGAGAAAGTGAAACTGAACAACAATGAATTGGAGACCATTCC  
 AAATCTGGGACCAAGTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA  
 ACATCTGAAAGAGTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATT  
 TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGGACAA  
 TTTGGCCAAACACTCTCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCAACCAAGATGTTTAAACT  
 GCCCCAAGTGAACATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG  
 TGCTCTGAAGTCTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAA  
 CATGGAAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCT  
 GCAGGAACCTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAG  
 TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAGCTTCCTTGGCCTAAGCTTACTAAATAC  
 ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTTCCGGGGGCTTTCCAGTTTAAAGACTTT  
 GGATCTGAAGAACAATGAAATTTCTTGGACTATTGAAGACATGAATGGTGTCTTCTCTGGGCTTGACAAACTGAG  
 GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCA  
 TCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAATT  
 GCATTTAAATACATCAAGCCTTTTGTGCGATTGGCAGTAAATGGCTCCACAGTGGGTGGCGGAAACAACCTT  
 TCAGAGCTTTGTAAATGCCAGTTGTGCCCATCTCAGCTGCTAAAAGGAAGAAGCAATTTTGTGTTAGCCCGAGA  
 TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCACGGTTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTT  
 CAATTTGAGTTTCTCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTTGTCTGGAAAAAAGACAATGA  
 ACTACTGCATGATGCTGAAATGGAAAATATGACACCTCCGGGCCCCAAGGTGGCGAGGTGATGGAGTATACCAC  
 CATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCTCAATCACTTTTGGTTT  
 ATCTACTCTGTCAAAGCCAAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCAT  
 CCGAGCTGGGGCCATGGCACGCTTGGAGTGTGCTGTGTTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA  
 TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGT  
 GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAAATGC  
 AACTCTGACTGTCTAGAAAACACCATCATTTTGTGGGCCACTGTTGGACCGAAGTGTAAACCAAGGGAGAAACAGC  
 CGTCTTACAGTGCAATTGTCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAGATGATAGCCCCATTGGTGGT  
 AACCGAGAGGCACCTTTTTCGAGCAGGCAATCAGCTTCTGATTATTTGGACTCAGATGTGATGCTGGGAA  
 ATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCAAC  
 CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGTGATCATAGC  
 CGTGGTTTGTCTGTGTTGGGACGTCACCTCGTGTGGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGA  
 TTGCAGCATTACCAACACAGATGAGACCAACTTGCCAGCAGATATTCCTAGTTATTTGTCTCTCAGGGAACGTT  
 AGCTGACAGGCAGGATGGGTACGTGTCTCAGAAAGTGGAAGCCACCACAGTTTGTCTCATCTTCAGGTGCTGG  
 ATTTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC  
 CACAGATCTGTTCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA  
 TCCTTTTGAACATATCATACAGGTTGCAGTCTTGACCAAGAAGCTTTTAAATGGACCACTATGAGCCAGTTA  
 CATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCTTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATC  
 GTGGCCTTTCATGTGAGGAAGCTACTTAACACTAGTTACTCTCAATGAAGGACCTGGAATGAAAAATCTGTG  
 TCTAAACAAGTCTCTTTTAGATTTTAGTGCAAAATCCAGAGCCAGCGTTCGGTTGCCTCGAGTAATCTTTTCATGGG  
 TACCTTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTCCAAC  
 AAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGAC  
 AGATTTTCAGGAAGAAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACCTACAGGACTCCAAATTTTCAGTC  
 TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACTACTACCTCAAGTGAACCTTTTATTTA  
 AAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAATGCTTTATTTATACAGAT  
 GAACCAAAATTACAAAAAGTTATGAAAATTTTATACTGGGAATGATGCTCATATAAGAATACCTTTTAAACTA  
 TTTTAACTTTGTTTTATGCAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGATTTT  
 TTATAATGCCAGATTTCTTTTTATGAAAATGAGTTACTAAAGCATTTTTAAATAATACCTGCCTTGTACCATTTT  
 TTAATAAGAGTTACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAA

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1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427
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**Signal sequence:**

**Transmembrane domain:**

N-glycosylation site.

**Glycosaminoglycan attachment site.**

amino acids 826-830

**Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

**Tyrosine kinase phosphorylation site.**

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

# FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG  
AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
TAAACCAGAGTTAGACCCGCGGGGGTTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCTCC  
CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAAGTATGTTTATTCTC  
TATAAAGGAGAAAGTGAGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT  
GGTGTGGTGGTGTCTTTCTTTCTTTTGAATTTCCACAAAGAGGAGAGAAATTAATAATACATCTGCAAGAAA  
TTTCAGAGAAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA  
TTTGTGCCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTCTTCTCATCAACCTCCTTTTTTTTAAAT  
TTTTATTCTTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACCTGGATTTCATCTGGATGTTGCT  
GTGATCAGTCTGAAATACAACCTGTTTGAATTCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAGAT  
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGGCCCTATTTGACCCCTGCTTGTGGTGCT  
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCAGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA  
CCAGTTCAAGGTGATTGTTGTGTTGCGAAAAACCTGCGTGAGGTTCGGATGGCATCTCCACCAACACACGGCT  
CTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTTCAAGCAGCTTGAGGCACTTGGAATCCT  
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA  
ACTCTTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTGTATACTTGTCTAACTGAAGGAGCTCTGGTT  
GCGAAACAACCCCATGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTTCGCGCCGACTAGACTTAGG  
GGAATTGAAAAGACTTTCATACATCTCAGAAGGTGCCTTTGAAGGTCTGTCCAACCTGAGGTATTTGAACCTTGC  
CATGTGCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAGCTGGATCTTTCTGGGAATCA  
TTTATCTGCCATCAGGCTGGCTCTTTCCAGGGTTTGATGCACCTTCAAAAACCTGTGGATGATACAGTCCAGAT  
TCAAGTGATTGAACGGAATGCCTTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC  
ATTACTGCCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTACATCACAACCCTTGGAACCTG  
TAACTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCGGTG  
TAACTCTCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCACATGCTATGCTCCGGT  
GATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGCGGCCTCCACATC  
CCTGACATCTGTATCTTGATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCGGATAGCTGT  
GCTCAGTGATGGTACGTTAAATTTTCAAAATGTAAGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA  
TTCCGTTGGGAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCCTACTCTTCTTACTTTTCT  
AACCGTCAAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCACTCC  
AGTGGTTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCACAGAGCACAAGGTGACAGAGAAAACCTT  
CACCATCCCAGTGACTGATATAAACAGTGGGATCCAGGAATTGATGAGGTGATGAAGACTACCAAAATCATCAT  
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCAATTTTCTACAAGATGAGGAAGCAGCACC  
TCGGCAAAACCATCACGCCCCAACCAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC  
CATGGAAAGCCACCTGCCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTT  
CAACCACACAACAACAGTTAAACACAATAAATTCAATACACAGTTTCAATGATGAACCGTTATTGATCCGAATGAA  
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACAATCAAAAAA  
GACAGTTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA  
AAAAGAAAAGAAATTTATTATTAAAAATCTATTGTGATCTAAAGCAGACAAAA

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## FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDLDELDSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTQDTGMYTCMVNSNSVGN  
TTASATLNVTAATTTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTKFTFTIPVTDINS GIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

### **Signal sequence:**

amino acids 1-44

### **Transmembrane domain:**

amino acids 523-543

### **N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

### **Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

### **N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

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# FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA  
TGAAAGGGCTTCGCCGCCGGGAGTAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACGCGACCGC  
GAGGGCGGGCGTGCACCTTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCGGGTGGGGTGGTGTGTC  
GACCTAGGCCGCTGGACCGGATGAGCGCGCGAGCCTCCGTGCGCGCGCGCGGGTGGGGTGGTGTGTC  
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGGTAGCCGCC  
GAGCGCCCATGCCCCACTACCTGCCGCTGCCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGCTAGCGCGTCTT  
CCCAGCCACTCCCGTCTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTCATCAAGGCAAGTTCC  
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAACCTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA  
GTCTCGGCAAAATATTACACTTCTCTCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAATGCATTTCCAGCCCTACAG  
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCAACACA  
CTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCAACCAAGATGTTTAAACTGCCCAACTGCAA  
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGGTGCTCTGAAGTCT  
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTTGGGGGCTGAGCAACATGGAAAATTTG  
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAATTCAT  
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCCTTGGCCTAAGCTTACTAAATACACTGCATTTGGG  
AACAACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGGGCTTTCCAGTTTAAAGACTTTGGATCTGAAGAAC  
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCACAAAATGAAGAACTGCAACAATTGCATTTAAATACA  
TCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCCAAGTGGGTGGCGGAAAACAACCTTTCAGAGCTTTGTA  
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAACCTTTTGGCTGTTAGCCAGATGGCTTTGTGTGT  
GATGATTTTCCCAAACCCAGATCACGGTTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTC  
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGTCTGGAAAAAGACAATGAACTACTGCATGAT  
GCTGAAATGGAAAATTTATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCACCATCCTTCGGCTG  
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCTCCAATCACTTTGGTTTATCCTACTCTGTCT  
AAAGCCAAGCTTACAGTAAATATGCTTCCCTCAATAGCAAGACCCCATGGATCTCACCATCCGAGCTGGGGCC  
ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGCACAGAC  
TTCCAGCTGCACGGGAGAGACGCATGCATGTGATGCCCGAGGATGACGTGTTCTTTATCGTGGATGTGAAGATA  
GAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTC  
CTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGTCCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCTTAACTGAATGACCAAGATGATAGCCCATTTGGTGGTAACCGAGAGGCAC  
TTTTTTGCAGCAGGCAATCAGCTTCTGATTATTGTGGACTGAGATGTCAGTGTGCTGGGAAATACACATGTGAG  
ATGTCTAACACCCTTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCCACTCCCACTGCCACTCCCT  
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTTGTGT  
GTGGTGGGCACGTCACTCGTGTGGGTGGTCTATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTACC  
AACACAGATGAGACCAACTTGGCAGCAGATATTCCTAGTTATTTGTCTCATCTCAGGGAACGTTAGCTGACAGGCAG  
GATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTTCTTACCA  
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTT  
CTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGATCCTTTTGAAACA  
TATCATACAGGTTGCAGTCTGACCAAGAACAGTTTTAATGGACCACTATGAGCCAGTTACATAAAGAAAAAG  
GAGTGCTACCCATGTTCTCATCCTTCAGAAAGATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT  
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC  
TCTTTAGATTTTATGTGCAAAATCCAGAGCCAGCGTGGCTCGAGTAATCTTTTCATGGGTACCTTTTGAAAA  
GCTCTCAGGAGACCTCACCTAGATGCCTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCCAAGAGCCTTTTAT  
TTGAAAGCTCATTCTTCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA  
GAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACACAGGACTCCAAATTTTCAGTCTTATGACTTGGAC  
ACATAGACTGAATGAGACCAAGGAAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTAAAGAGAGAGAAT  
CTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTTATACAGATGAACCAAAATTAC  
AAAAAGTTATGAAAAATTTTATACCTGGGAATGATGCTCATATAAGAATACCTTTTTTAACTATTTTTTAACTTTG  
TTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTATTTTATGTATTTTATAATGCCAGA  
TTTCTTTTTTATGGAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTTTTAAATAGAATT  
ACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAA

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# FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR  
 KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT  
 LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
 FDNLANTLLVLKLNRRNRI SAIPPKMFKLPLQHLLELNRNKIKNVDGLTFQGLGALKSLKMQR  
 NGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
 QKLSELDLTFNHL SRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS  
 WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSOMK  
 KLQQLHLNTSSLLCDCQLKWL PQWVAENNFSQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF  
 PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQGG  
 VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
 RLECAAVGHPAPQIAWQKGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
 GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF  
 FAAGNQLLIIVDSVDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA  
 TVGVVIIAVVCCVVGTSLVVVVVIYHTRRRNEDCSITNTDETNL PADIPSYLSSQGT LADRQ  
 DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
 LKGNVYGS DPFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS  
 HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
 SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
 1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

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# FIGURE 107

CAAAACCTTGCCTCGCGGAGAGCGCCAGCTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC  
 TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
 CTGCTCCACGAGGCGCCACTGGTGTGAACCGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATA  
 GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGCTCATGGTGAGCAAGGAGGCGGCTGATCTGCAG  
 GCGCACAGCATTCCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT  
 TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGCCGGGTGCTGC  
 TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGGCGTGAGGGCCCCAGGATTTGGCCGAA  
 GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGTGGTACTGAGCCCTGAGG  
 AGCCCGGGCCTGGCCCAGCCGCGGTGAGTGCCTGGGACCTGTGCTTGGCGTGAGGGCCCCAGGATTTGGCCGAA  
 GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACCAACCAGC  
 TGGAAAAGATCTACCCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA  
 CTTCCCGAGGGCTCCAGAGAAGGCGTTTGGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
 TGACCTTGGCACCCCGCTTCTGCAAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT  
 ATGGGCTCACCTTTGGCCAGAAGCCAACTTGGAGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC  
 TGCCGGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC  
 CCAAGCACCTGCGCCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT  
 TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACCAACTACCTGACTGACGAGGGCCTGGACAACGAGA  
 CTTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC  
 CGCGCAGCCTGGTGTGCTGCACTTGGAGAAGAAGCCATCCGGAGCGTGACGCGAATGTGCTGACCCCCATCC  
 GCAGCCTGGAGTACCTGTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCACTGGCCTTCCAGGGCC  
 TCAAGCGGTTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTGCCAGTGCCCTGCCTCGCCGCGTGC  
 GCACCTCATGATCCTGCACAACCAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGG  
 AGCTCAACCTCAGCTACAACCGCATCACAGCCACAGGTGCACCGGACGCTTCCGCAAGCTGCGCCTGCTGC  
 GCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG  
 TCAAGCGCAATGAGCTGGCTGCCTTGGCAGGAGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
 CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTGGACCTCGCCCATCTGCAGCTGTGGACA  
 TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGTAGTACCTGTACCTGCAGAACAACA  
 AGATTAGTGCCTGCGCGCCCAATGCCTTCGACTCCACGCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAAGC  
 TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT  
 TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGG  
 AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTCTTTTCTGC  
 AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA  
 TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCCACGGCCAGACACATGC  
 ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACCTCCAAACCACACAGTCTCTGTACACAC  
 CCCCCTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCCCTGCCCTGGCACACACAGGCACCCA  
 TTCCCTCCCCCTGTGACATGTGTATGCGTATGCATACACACCACACACACACATGCACAAGTCATGTGCGAA  
 CAGCCCTCAAAGCCTATGCCACAGACAGCTCTTGGCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT  
 GTCCATCTGTCCGTCCGTTCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCCTCT  
 GGAACCTCAAAAAGCTGGCTTTTATTCCTTTCCCATCCTATGGGGACAGGAGCCTTCAAGACTGCTGGCCTGGCC  
 TGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGTAAAGAGTCCCTGCCACGCCCTGGCAGGACA  
 CAGGCACTTTTCAAATGGGCAAGCCAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG  
 CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT  
 GTTCTTCAGGCCTGTGGGGGAAGTTCCGGGTGCCTTTATTTTATTTCTTTCTAAGGAAAAAATGATAAAAAT  
 CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAAA

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**Q. 1. What is the purpose of the study?**

**Signal sequence:**

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

[illegible][illegible]

$\frac{1}{2} \frac{d}{dt} \int_{\mathbb{R}^n} |u|^2 dx = \int_{\mathbb{R}^n} u \frac{du}{dt} dx = \int_{\mathbb{R}^n} u \left( -\frac{1}{2} \Delta u \right) dx = -\frac{1}{2} \int_{\mathbb{R}^n} u \Delta u dx = \frac{1}{2} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \frac{1}{2} \int_{\mathbb{R}^n} |\nabla u|^2 dx = \frac{1}{2} \int_{\mathbb{R}^n} |\nabla u|^2 dx$

**Signal sequence:**

N-glycosylation site.

Casein kinase II phosphorylation site.

**Tyrosine kinase phosphorylation site.**

N-myristoylation site.

**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

**EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCTTTAGATTGTGA  
AATGTGGCTCAAGGTCTTCACAACCTTTCCTTTCTTTTGCAACAGGTGCTTGCTCGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTGAGGCCCTTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC  
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTGAGGGAAATGGAACCTCTATCTGCCAGTCA  
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCATCCTCCCT  
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTGAGGAACCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT  
TGACCTTGAGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAAATCATTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATT  
ATATCCATGTGTCTTCTCTTCTATGAAAAAATATCAACCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT  
GTATGAAGTTATTCAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACTTTCATGG  
GCTAAACAGTACATTCGAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAGT  
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA  
TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
TGTGGAACCTTTACATTGTTTCGATTTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG  
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA  
CAAAGTAATAAGGATGGTTGTCACAAAAACAAAACCTATGCCTTCTCTTTTTTTTCAATCACC  
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA  
TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGCTTTTAAAAA

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## FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNRGPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFDPVSGVSRIPSRVSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

03903525.07404



## FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGACAGTTCCTGGCAGTCCTGGTGCTGTT  
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT  
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC  
TTCCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT  
GTTTTTGCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC  
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAAT  
TATTATCAGAATCTGCACAACCTTTGAAAAAGTGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCACAGAATGC  
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAG  
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCATTTTGGTTTGAAGTG  
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA  
CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG  
GTTTAAATAGTTCTCTAATTTTGAATAATCGTGCCAAGCAATAAGATTTATGTATATTTGT  
TTAATAATAACCTATTTCAAGTCTGAGTTTTGAAAATTTACATTTCCCAAGTATTGCATTAT  
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTGATATAATTTTCTCTG  
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG  
AAATGTGTATTTTCAGTGACAATTTCTGTGGTCTTTTTAGAGGTATATTCCAAAATTTCTGT  
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAAGTTCATGGTATTCTCTGATTC  
CAACAAAGTTTGATTTTCTCTGTATTTTTCTTACTTACTATGGGTACATTTTTTATTTTT  
CAAATTGGATGATAATTTCTTGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTT  
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAATTT  
TTGGCCACTTTTTTTCAGATTTTACATCATTCTTGCTGAACTTCAACTTGAAATTTGTTTTTT  
TTTCTTTTTTGGATGTGAAGGTGAACATTTCTGATTTTTTGTCTGATGTGAAAAAGCCTTGGTA  
TTTTACATTTTGAATTTCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAG  
CATCTTCTTGATATATGTCTTAAATGTATTTTTGTCTCATATACAGAAAGTTCTTAATTGAT  
TTTACAGTCTGTAATGCTTGATGTTTTAAATAATAACATTTTTTATATTTTTTAAAGACAA  
ACTTCATATTATCCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTTCACAGGTAAAA  
GTCAGTAGGATGGAACATTTTAGTGTATTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT  
CACCTTAAAGAAGGGGGGAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC  
AATTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG  
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT  
AAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT  
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAAAAA

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$$\begin{pmatrix} \mathbb{C}^{n_1} & \mathbb{C}^{n_1 \times n_2} & \mathbb{C}^{n_2} & \mathbb{C}^{n_2 \times n_3} & \mathbb{C}^{n_3} \\ \mathbb{C}^{n_2 \times n_1} & \mathbb{C}^{n_2} & \mathbb{C}^{n_2 \times n_3} & \mathbb{C}^{n_3} & \mathbb{C}^{n_3 \times n_4} \\ \mathbb{C}^{n_3} & \mathbb{C}^{n_3 \times n_4} & \mathbb{C}^{n_4} & \mathbb{C}^{n_4 \times n_5} & \mathbb{C}^{n_5} \end{pmatrix} \mapsto \begin{pmatrix} \mathbb{C}^{n_1} & \mathbb{C}^{n_1 \times n_2} & \mathbb{C}^{n_2} \\ \mathbb{C}^{n_2} & \mathbb{C}^{n_2 \times n_3} & \mathbb{C}^{n_3} \\ \mathbb{C}^{n_3} & \mathbb{C}^{n_3 \times n_4} & \mathbb{C}^{n_4} \end{pmatrix}$$

**Signal sequence:**

**Transmembrane domain:**

Casein kinase II phosphorylation site.

**Tyrosine kinase phosphorylation site.**

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

[illegible]

CGGAGTGTCCAGCTGCGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCCTTCTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG AAGGTCCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCCTTACCTCTATTG GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCCTGTGAATGCCTACAAACTGG TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGTCAGGACTCAGCTGCA GGTTTTATCGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA GAGGGGAACTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCCTGCTC TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTGGG GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA TCGTCAGGTACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCTACTGTGCGCAGCTA CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATC GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTGTAGAAGCTG GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCCTGCCC TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTTCCCCCTTCTGGTC CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTTCTATCAGGCT GATTTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT GTGACTGAAGTCCCAGCCCTTCCATTGAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTTAT GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

## FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYIILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAALMRLQDTYRLDPGTISRGEIPGTYQAMLSVDDCFGMGRSAYNEGDYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEEEREKTLTNQTEAELATPEGIYERPVLDYLPERDVYESLCRGEQVGLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPIVRYDVMSEDEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHDFS  
RRPFDGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEQDYL  
TRHAACPVLVGCKWVSNKWFHERGQEFRLPCGSTVD

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 115-119, 264-268

### **Glycosaminoglycan attachment site.**

amino acids 490-494

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

### **Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

### **Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

### **N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

### **Leucine zipper pattern.**

amino acids 213-235

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# FIGURE 117

GCAGTATTGAGTTTTACTTCCTCCTCTTTTTAGTGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT  
TTCATTTATTACCGTTTTGGCTGGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA  
AGACAGGACAATCTTCTTGGGGATGCTGGTCCTGGAAGCCAGCGGGCCTTGCTCTGTCTTTGGCCTCATTGACCC  
CAGGTTCTCTGGTTAAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC  
CCTGGGGCACCACCTGGCAGGGCCTACCACCATGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC  
CCCTCATCTTAGGGCTGTCTCTGGGGTGACGCTGAGCCTCCTGCGGGTTTCTGGATCCAGGGGAGGGAGAAG  
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG  
ATGAAGACTTCAAACCCCGGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC  
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCCGAGCTACACTGTCCA  
CTTTGGCCGTGGCTGTGAACCGTACGGTGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGCGGGGG  
CCCGGGCTCCAGCAGGGATGAGGTGGTGTCTCATGGGGATGAGCGGCCCGCCTGGCTCATGTGAGAGCCCTGC  
GCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTTCATCATGAGGATGACACATATGTGAGGCCC  
CCCGCCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTATTG  
GCGCAGGCGAGCAGGCCCCGCTACTGTGATGGGGGCTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCTGC  
GGCCACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCCCCTCTGACGAGTGGCTTGGACGCTGCCTCATTG  
ACTCTCTGGGCGTCGGCTGTGTCTCAGCAGCAGGGGCGAGCAGTATCGCTCATTTGAACTGGCCAAAAATAGGG  
ACCCTGAGAAGGAAGGGAGCTCGGCTTTCTGAGTGCCTTCGCGGTGACCCCTGTCTCCGAAGGTACCCCTCATGT  
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAACCTGCAGGCTCAGA  
TCCGGAACCTGACCGTGCTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTCA  
CACCACACTCTCGCTTTGAGGTGCTGGGCTGGGACTACTTCACAGAGCAGCACACCTTCTCCTGTGAGATGGGG  
TCCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
ATCGGCGCTATCAGCCCCGCTTCCGCTTCCAGGAGTGTGTGACACAGCGTGGGCACCGGGGGCCCTGGCTCGCA  
GGGTCAGCCTGCTGCGGCCACTGAGCCGGGTGGAAATCCTACCTATGCCCTATGTCACTGAGGCCACCCGAGTGC  
AGCTGGTGCTGCCACTCCTGGTGGCTGAAGCTGCTGCAGCCCCGGCTTTCTCGAGGCGTTTGCAGCCAATGTCC  
TGGAGCCACGAGAATGCAATTGCTCACCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG  
ACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCCTGGGACGAGGCTGGCCTGGCTCG  
CTGTGCGAGCAGAGGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCCCTGTGGACACTCTCT  
TCTTCTTACCACCGTGTGGACAAGGCCTGGGCCCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT  
GGCAGGCCTTCTTTCCAGTCCATTTCCAGGAGTTCAATCCTGCCCTGTGACACAGAGATCACCCCCAGGGCCCC  
CGGGGGCTGGCCCTGACCCCCCTCCCCTCCTGGTGCTGACCCCTCCCGGGGGCTCCTATAGGGGGGAGATTTG  
ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGGCCGAGCCCGGCTGGCAGGTGAAC  
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTCTCCTCCGGTCTCAGGGCTCC  
ACCTCTTTCGGGCGGTAGAGCCAGGGCTGGTGAGAGTTCTCCCTGCGAGACTGCAGCCACGGCTCAGTGAAG  
AACTCTACCACCGCTGCCGCCCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTCTTTG  
AGCAGGAGCAGGCCAATAGCACTTAGCCCCGCTGGGGGCCCTAACCTCATTACCTTTCTTTGTCTGCCTCAGCC  
CCAGGAAGGGCAAGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAAATGTTATTAA  
ACATGTCTTCTGCC

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## FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPD SRARLD  
 QSDDFKPRIVPYRDPNKPYPKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV  
 AHHPRLLYFTGQRGARAPAGMQVVS HGDERP A WLMSETLRHLHTHFGADYD WFFIMQDDTY  
 VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
 DILSARPD EWLGRCLIDSLGVGCVSQHQQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE  
 GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLT VLTPEGEAGLSWPVGLPAPFTPHSRFEV  
 LGWDYFTEQHTFSCADGAPKCP LQGASRADVGDALETALEQLNRRYQPR LRFQKQRL LNGYR  
 RFD PARGMEYTL D L L L E C V T Q R G H R R A L A R R V S L L R P L S R V E I L P M P Y V T E A T R V Q L V L P L L  
 VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAA AELERRYPG  
 TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLT TVWTRPGPEVLNRCRMNAISGWQAFFP  
 VHFQEFNPALSPQRSPPGPPGAGDP PPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA  
 RARLAGELAGQEEEEALEGLEVMDFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR  
 CRLSNLEGLGGRAQLAMALFEQE QANST

**Signal sequence:**

amino acids 1-15

**Transmembrane domain:**

amino acids 489-507

**N-glycosylation site.**

amino acids 121-125, 342-346

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

**Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
 399-403, 409-413, 473-477, 729-733, 748-752

**Tyrosine kinase phosphorylation site.**

amino acids 736-743

**N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
 558-564, 651-657, 657-663, 672-678

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

**Cell attachment sequence.**

amino acids 247-250

00903925 07404

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG  
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAACC  
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG  
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTG  
GTTCTTCCTTGACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA  
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAATCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCCAGAAAAGTGCTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTTTCAATATGGCTGTTACTTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTTGGGCATATTTTCAAT  
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA  
TACAGCTGTATGTTTTCTTTTTCTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTTTTAAATGAGGGTGGTTTTTTTTCTTTAAACACATGAACATTGTAAATG  
TGTTGGAAAGAAGTGTTTTAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT  
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTGCTGATTGGTT  
AAAAAATTTTAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT  
AAGCCTCCCCAAGTTCCAATGGATTTGCCTTCTCAAAATGTACAACCTAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAAT

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**COPIES OF THE REPORT IN FULL ARE:**

**Signal sequence:**

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250



## FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG  
AAAAAGAGAGAGAGAGAGAAACAAAAAACCAAAGAGAGAGAGAAAAATGAATTCATCTAAATCAT  
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT  
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT  
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT  
ACAATTATGGATCAGGTTCAAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC  
AGCTGCTACTTCTTTTCTACTGACACCATTTCTGCGGCTTAAGTTTAAAGAAGTCTCAGC  
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCTTACAAGA  
AACCTAAAATGAGAGAGTTTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAA  
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA  
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA  
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG  
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA  
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACCTTCAAAGGACTTC  
ATAAGTATTTGTTACTCTGATACAAATAAAAAATAAGTAGTTTAAATGTTAAAAAAAAAAAA  
AA  
AAAAA

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## FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDCATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

**Signal sequence:**

amino acids 1-42

**N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

**Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

**N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

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# FIGURE 123

GGGACTACAAGCCGCGCCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACGTCTTGCATCATTACGGATTTCG  
AGACAAGTGACCCAGGATCGAGTGAAGAAATTAAGATGAACAAACCACATATGTGTTTTTGGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCTGTCAGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
ACTCAGCCCTTTATCGCTGTGAGGTCTGTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCGGCTCACTACAGCTGGTATCGCAATGATGTACCAGTGGCCACGGATT  
CCAGAGCCAATCCCAGATTTGCAATTTCTTCTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCAGTGTCTG  
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTCTGGTGTCTTGTCTACTGGCCCTGA  
TCAGTTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTTG  
TGATCTGAGACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTGAGAAGCTTTTCGTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTCTTAATCTGTTTCTGGCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGTCTACGTAAACGCGCGTGTGGGCTGTGAAGCCAGCATGTTCACTCTGGTCTGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTTCATCGGCCACAGACACCACCGCAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTGTCAGTGTCCATTGTGGAGAAGCTTTTTGGATCAGCATTTTGTAAAAACAACCAAAATCAGGAAG  
GTAAATTGGTTGCTGGAAGAGGATCTTGCCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGATTAAAGGAAA  
ACCTTCGCTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTATTATTTATAAAATTT  
TACATCTAAATTTTTGCTAAGGATGTATTTTGATTATTGAAAAGAAAATTTCTATTTAAACTGTAAATATATTGT  
CATACAATGTAAATAACCTATTTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAAGAGTATTTTACCCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTCTTTTCT  
CACACAAGTTTTCAGCTTTTTCACAAGGGAACCTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
CCAGTCAGCTCCTGGGGTTCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGGCCTGGCAGTGGCTGTGTCCAGTGAGCTTTACTCACGTGGCCCTTGCTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCAGAAAATAGGGCCCCCAATGCTATTTTTTTTTTAAAGTTTGTAAATTATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT  
CCCAGTGTCTCTTTTGGCACAGAGAAAAGCACCCAGAGGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGGAGGAAAG  
TGAAACGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTTTCATCCGCCGAGACACTGCTCCATT  
TGTGGGGGGACATTAGCAACATCACTCAGAAAGCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGACTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTTTATCTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCGCGAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGTCTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCTCAGCGTTGGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTCTAGTGATAGGGTAGCCTTATTGCCCCCTCTTCTTATACCTTAAACCTTCTACACTAGTGCCA  
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTGTACTAACACACCGTAATTTGGCATTGTGTTAAC  
CTCATTATATAAAGCTTCAAAAAACCCA

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MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESEGHPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEEMEVDNLNIGGIIGG  
VLVVLAVALALITLGICAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267